WHAT IS CLAIMED IS:

1. A method of identifying an exon in a eukaryotic genomic fragment, the method comprising:

expressing a population of subsequences of the genomic fragment in a phage display library, wherein the population comprises protein-encoding subsequences and noncoding subsequences;

screening the phage display library with a binding partner to identify an expressed subsequence that specifically binds to the binding partner; and

mapping the expressed subsequence to the physical location in the genomic fragment, thereby identifying the exon.

2. The method of claim 1, wherein the binding partner is an antibody, an enzyme or a receptor.

3. The method of claim 2, wherein the binding partner is an antibody.

4. The method of claim 3, wherein the antibody is a single chain antibody.

5. The method of claim 1, wherein the binding partner is expressed by a phage display library.

6. The method of claim 5, wherein the phage display library is an antibody phage display library generated using mRNA isolated from a stimulated B cell or a naïve B cell.

7. The method of claim 6, wherein mRNA isolated from the stimulated B cell is mRNA isolated from a stimulated splenic B cell that is isolated from an animal immunized with a composition comprising the protein epitope encoded by the genomic sequence or a nucleic acid encoding the protein epitope.

8. The method of claim 1, wherein the expressed subsequences are from about 100 base pairs to about 300 base pairs in length.

9. The method of claim 1, wherein the genomic fragment is from a mammalian genome.

10. The method of claim 1, further wherein the exon is abnormally expressed in a cell of an individual with a disease or condition.

11. The method of claim 10, wherein the cell has a genomic translocation involving the exon sequence.

12. The method of claim 10, wherein the disease is cancer.

13. The method of claim 1, further comprising a step of enriching for phage expressing subsequences of the genomic fragment that are exons.

14. The method of claim 13, wherein the step of enriching comprises incubating the phage library with a binding partner specific for a peptide encoded by a subsequence that does not encode a peptide *in vivo*, and removing phage expressing the peptide from the library.

15. The method of claim 14, wherein the subsequence that does not encode a peptide *in vivo* is a repetitive sequence.

16. The method of claim 15, wherein the repetitive sequence is an Alu sequence or a Kpn sequence.

17. A phage display library comprising phage that express a population of subsequences of a eukaryotic genomic fragment, wherein the population comprises protein coding subsequences and noncoding subsequences.

18. The phage display library of claim 11, wherein the eukaryotic genomic fragment is from a mammalian genome.

19. The phage display library of claim 17, wherein the library is constructed using a pBPM-1 vector.

20. The phage display library of claim 17, wherein the expressed subsequences are from about 100 base pairs to about 300 base pairs in length.

21. A phage expression vector comprising a polylinker region, an out-of-frame pIII gene, and at least one non-pallindromic rare cutting restriction enzyme site located

in the polylinker site, wherein the non-pallindromic rare cutting restriction enzyme site is not located outside the polylinker region, and a selection tag encoding sequence.

22. The phage expression vector of claim 21, wherein the non-pallindromic rare cutting restriction enzyme site is an SfiI site.

23. The phage expression vector of claim 21, wherein the selection tag is an epitope tag selected from the group consisting of a polyhistidine tag or a myc tag.

24. The phage expression vector of claim 21,wherein the selection tag is an antibiotic resistance polypeptide.

25. A method of identifying an exon in a genomic fragment, the method comprising:

expressing a population of subsequences of the genomic fragment in a phage display library, wherein the population comprises protein-encoding subsequences and noncoding subsequences;

enriching for phage expressing subsequences of the genomic fragment that are exons;

screening the phage display library with a binding partner to identify an expressed subsequence that specifically binds to the binding partner; and

mapping the expressed subsequence to the physical location in the genomic fragment, thereby identifying the exon.

26. The method of claim 25, wherein the step of enriching comprises incubating the phage library with a binding partner specific for a peptide encoded by a subsequence that does not encode a peptide *in vivo*, and removing phage expressing the peptide from the library.

27. The method of claim 26, wherein the subsequence that does not encode a peptide *in vivo* is a repetitive sequence.

28. The method of claim 25, wherein the expressed subsequences are from about 100 base pairs to about 300 base pairs in length.